

FIG. 15 CONTINUED

ClaI
 |
 AAGT G G A A

361 TGGGGGATGTGAAGGAAATCAGAAATCGATTGAGTCCCTCGAAGAATGCAAGAAGATGTG 420
 -----+-----+-----+-----+-----+-----+-----+
 ACCCCCTACACTTCCTTTAGTCTTAGCTAAACTCAGGGAGCTTCTTACGTTCTTCTACAC
 GlyGlyCysGluGlyAsnGlnAsnArgPheGluSerLeuGluGluCysLysLysMetCys -
 75

421 T AA A T T
 CACCCGCGACAACGCAAACAGGATTATAAAGACAACATTGCAACAAGAAAAGCCAGATTT 480
 -----+-----+-----+-----+-----+-----+-----+
 GTGGGCGCTGTTGCGTTTGTCTAATATTTCTGTTGTAACGTTGTTCTTTTCGGTCTAAA
 ThrArgAspAsnAlaAsnArgIleIleLysThrThrLeuGlnGlnGluLysProAspPhe -

481 CTGCTTTTTTGAAGAAGATCCTGGAATATGTGCGAGGTATATTTACCAGGTATTTTTTATAA 540
 -----+-----+-----+-----+-----+-----+-----+
 GACGAAAAACCTTCTTCTAGGACCTTATACAGCTCCAATATAATGGTCCATAAAAAATATT
 CysPheLeuGluGluAspProGlyIleCysArgGlyTyrIleThrArgTyrPheTyrAsn -

541 CAATCAGACAAAACAGTGTGAACGTTTCAAGTATGGTGGATGCCTGGGCAATATGAACAA 600
 -----+-----+-----+-----+-----+-----+-----+
 GTTAGTCTGTTTGTGCACACTTGCAAAGTTCATACCACCTACGGACCCGTTATACTTGTT
 AsnGlnThrLysGlnCysGluArgPheLysTyrGlyGlyCysLeuGlyAsnMetAsnAsn -

601 TTTTGAGACACTGGAAGAATGCAAGAACATTTGTGAAGATGGTCCGAATGGTTTCCAGGT 660
 -----+-----+-----+-----+-----+-----+-----+
 AAAACTCTGTGACCTTCTTACGTTCTTGTAAACACTTCTACCAGGCTTACCAAAGGTCCA
 PheGluThrLeuGluGluCysLysAsnIleCysGluAspGlyProAsnGlyPheGlnVal -

661 GGATAATTATGGAACCCAGCTCAATGCTGTGAATAACTCCCTGACTCCGCAATCAACCAA 720
 -----+-----+-----+-----+-----+-----+-----+
 CCTATTAAATACCTTGGGTCGAGTTACGACACTTATTGAGGGACTGAGGCGTTAGTTGGTT
 AspAsnTyrGlyThrGlnLeuAsnAlaValAsnAsnSerLeuThrProGlnSerThrLys -

721 GGTTCCCGAGCCTTTTTGAATTTACGGTCCCTCATGGTGTCTCACTCCAGCAGACAGAGG 780
 -----+-----+-----+-----+-----+-----+-----+
 CCAAGGGTCGGAAAACTTAAAGTGCCAGGGAGTACCACAGAGTGAGGTCGTCTGTCTCC
 ValProSerLeuPheGluPheHisGlyProSerTrpCysLeuThrProAlaAspArgGly -

781 ATTGTGTCGTGCCAATGAGAACAGATTCTACTACAATTCAGTCATTGGGAAATGCCGCC 840
 -----+-----+-----+-----+-----+-----+-----+
 TAACACAGCACGGTTACTCTTGTCTAAGATGATGTTAAGTCAGTAACCCTTTACGGCGGG
 LeuCysArgAlaAsnGluAsnArgPheTyrTyrAsnSerValIleGlyLysCysArgPro -

FIG. 15 CONTINUED

ATTTAAAGTACAGTGGATGTGGGGGAAATGAAAACAATTTTACTTCCAAACAAGAATGTCT
 841 -----+-----+-----+-----+-----+-----+-----+ 900
 TAAATTCATGTCACCTACACCCCTTTACTTTTGTATAAATGAAGGTTTGTCTTACAGA
 PheLysTyrSerGlyCysGlyGlyAsnGluAsnAsnPheThrSerLysGlnGluCysLeu -
 GAGGGCATGTAAAAAAGGTTTTCATCCAAAGAATATCAAAAGGAGGCCTAATTAAACCAA
 901 -----+-----+-----+-----+-----+-----+-----+ 960
 CTCCCGTACATTTTTTCCAAAGTAGGTTTCTTATAGTTTCTCCGGAATTAATTTTGGTT
 ArgAlaCysLysLysGlyPheIleGlnArgIleSerLysGlyGlyLeuIleLysThrLys -
 C terminus of Ala-TFPI coding sequence
 AAGAAAAAGAAAGAAGCAGAGAGTGAAAATAGCATATGAAGAAATTTTTGTAAAAATAT
 961 -----+-----+-----+-----+-----+-----+-----+ 1020
 TTCTTTTCTTTCTTCGTCTCTCACTTTTATCGTATACTTCTTTAAACAATTTTATA
 ArgLysArgLysLysGlnArgValLysIleAlaTyrGluGluIlePheValLysAsnMet -
 Stop HindIII
 TGA^^^AAGCTT (in pMON6655)
 Translation Termination
 HindIII ClaI EcoRI EcoRV P22 term delta
 GTAATAAAAGCTTATCGATGATAAGCTGTCAAACATGAGAATTCGATATCAACGCAACGA
 1021 -----+-----+-----+-----+-----+-----+-----+ 1080
 CATTATTTTTCGAATAGCTACTATTTCGACAGTTTGTACTCTTAAAGCTATAGTTGCGTGTCT
 EndEnd
 EcoRV EcoRI
 GCCAGCCGAAGCTGGGTCGTTGCGTTGATATCGAATTC
 1081 -----+-----+-----+-----+-----+-----+-----+ 1118
 GGGTCGGCTTCGACCCAGCAACGCAACTATAGCTTAAG